

Ponsant

Sequences producing significant alignments:		Score (bits)	E Value	
gi 23238206 ref NM_014452.3 	Homo sapiens tumor necrosis fa...	417	e-114	GIUE
gi 37181727 gb AY358304.1 	Homo sapiens clone DNA52594 DR6-...	417	e-114	GIU
gi 7022799 dbj AK001504.1 	Homo sapiens cDNA FLJ10642 fis, ...	417	e-114	GIUE
gi 6478163 emb AL096801.18 	HSJ181J13 Human DNA sequence fro...	417	e-114	
gi 15880636 emb AJ336218.1 	HSA336218 Homo sapiens genomic s...	409	e-111	
gi 15880407 emb AJ335989.1 	HSA335989 Homo sapiens genomic s...	325	3e-86	
gi 15868604 emb AJ324225.1 	HSA324225 Homo sapiens genomic s...	269	2e-69	
gi 34783298 gb BC017730.2 	Homo sapiens tumor necrosis fact...	166	3e-38	GIUE
gi 3549262 gb AF068868.1 	Homo sapiens TNFR-related death r...	144	1e-31	GIUE
gi 32880108 gb BT009883.1 	Synthetic construct Homo sapiens...	144	1e-31	
gi 30583678 gb BT007420.1 	Homo sapiens tumor necrosis fact...	144	1e-31	GIUE
gi 55626753 ref XM_518523.1 	PREDICTED: Pan troglodytes tum...	136	3e-29	
gi 15870715 emb AJ326321.1 	HSA326321 Homo sapiens genomic s...	122	5e-25	
gi 34874517 ref XM_236992.2 	Rattus norvegicus similar to d...	96	4e-17	GIU
gi 31341673 ref NM_178589.2 	Mus musculus tumor necrosis fa...	88	9e-15	GIU
gi 26335926 dbj AK043823.1 	Mus musculus 10 days neonate co...	88	9e-15	GIU
gi 16741136 gb BC016420.1 	Mus musculus tumor necrosis fact...	86	4e-14	GIUE
gi 26329206 dbj AK033529.1 	Mus musculus adult male colon c...	82	6e-13	GIU
gi 15877202 emb AJ332784.1 	HSA332784 Homo sapiens genomic s...	52	6e-04	
gi 17432071 emb AL646086.1 	Ralstonia solanacearum GMI1000 ...	44	0.15	

gi 56178122 gb AE017340.1 	Idiomarina loihiensis L2TR, comp...	42	0.59	
gi 22795236 gb AC127460.2 	Homo sapiens chromosome 5 clone ...	42	0.59	
gi 14625084 gb AC084380.8 	AC084380 Oryza sativa chromosome ...	42	0.59	
gi 33879154 gb BC021165.2 	Homo sapiens zinc finger protein...	40	2.3	GU
gi 33870187 gb BC013011.2 	Homo sapiens zinc finger protein...	40	2.3	GU
gi 34871182 ref XM_343874.1 	Rattus norvegicus similar to f...	40	2.3	GU
gi 25453488 gb AY057439.2 	Azotobacter vinelandii GroEL (gr...	40	2.3	
gi 52421840 gb CP000011.1 	Burkholderia mallei ATCC 23344 c...	40	2.3	
gi 34222201 ref NM_032772.3 	Homo sapiens zinc finger prote...	40	2.3	GU
gi 52211453 emb BX571966.1 	Burkholderia pseudomallei strai...	40	2.3	
gi 34534651 dbj AK127647.1 	Homo sapiens cDNA FLJ45745 fis,...	40	2.3	GU
gi 21751602 dbj AK092897.1 	Homo sapiens cDNA FLJ35578 fis,...	40	2.3	GU
gi 21106326 gb AE011651.1 	Xanthomonas axonopodis pv. citri...	40	2.3	G
gi 33871437 gb BC011625.2 	Homo sapiens zinc finger protein...	40	2.3	GU E
gi 20303531 gb AC010997.12 	Homo sapiens chromosome 10 clon...	40	2.3	
gi 15875552 emb AJ331134.1 	HSA331134 Homo sapiens genomic s...	40	2.3	
gi 18653743 gb AC012236.12 	Homo sapiens chromosome 15, clo...	40	2.3	
gi 29608854 dbj AP005042.1 	Streptomyces avermitilis genom...	40	2.3	
gi 24646031 ref NM_141841.1 	Drosophila melanogaster CG1053...	38	9.4	GU
gi 23171004 gb AE003692.3 	Drosophila melanogaster chromoso...	38	9.4	
gi 31208238 ref XM_313086.1 	Anopheles gambiae ENSANGP00000...	38	9.4	GU
gi 50947384 ref XM_483220.1 	Oryza sativa (japonica cultiva...	38	9.4	G
gi 51965001 ref XM_507285.1 	PREDICTED Oryza sativa (japoni...	38	9.4	U
gi 50929414 ref XM_474235.1 	Oryza sativa (japonica cultiva...	38	9.4	G
gi 34896883 ref NM_184897.1 	Oryza sativa (japonica cultiva...	38	9.4	G
gi 37534057 ref NM_196349.1 	Oryza sativa (japonica cultiva...	38	9.4	G
gi 50937328 ref XM_478192.1 	Oryza sativa (japonica cultiva...	38	9.4	G
gi 28269488 gb AC092781.6 	Oryza sativa chromosome 3 BAC OS...	38	9.4	
gi 29789306 ref NM_057200.1 	Rattus norvegicus kinesin fami...	38	9.4	GU
gi 31431860 gb AE017090.1 	Oryza sativa (japonica cultivar-...	38	9.4	
gi 32489031 emb AL606999.3 	OSJN00127 Oryza sativa genomic D...	38	9.4	
gi 42469651 emb BX820650.1 	CNS0AA3D Arabidopsis thaliana Fu...	38	9.4	U
gi 42468881 emb BX818953.1 	CNS0A9UM Arabidopsis thaliana Fu...	38	9.4	U
gi 42468460 emb BX820086.1 	CNS0A9DI Arabidopsis thaliana Fu...	38	9.4	U
gi 42468388 emb BX819814.1 	CNS0A9FM Arabidopsis thaliana Fu...	38	9.4	U
gi 42468355 emb BX819698.1 	CNS0A9GB Arabidopsis thaliana Fu...	38	9.4	U
gi 22296994 gb AC105101.8 	Homo sapiens chromosome 18, clon...	38	9.4	
gi 38257164 gb AC109601.9 	Oryza sativa chromosome 3 BAC OS...	38	9.4	
gi 40786619 gb AC096856.7 	Oryza sativa chromosome 3 BAC OS...	38	9.4	
gi 42408124 dbj AP004190.3 	Oryza sativa (japonica cultivar...	38	9.4	
gi 21428993 gb AY119562.1 	Drosophila melanogaster GM13228 ...	38	9.4	U
gi 13421727 gb AE005727.1 	Caulobacter crescentus CB15 sect...	38	9.4	G
gi 21387210 gb AY114690.1 	Arabidopsis thaliana proline imi...	38	9.4	GU
gi 37988923 dbj AK119300.1 	Oryza sativa (japonica cultivar...	38	9.4	U
gi 21111436 gb AE012143.1 	Xanthomonas campestris pv. campe...	38	9.4	G
gi 37806382 dbj AP006064.3 	Oryza sativa (japonica cultivar...	38	9.4	
gi 9947599 gb AE004591.1 	Pseudomonas aeruginosa PA01, sect...	38	9.4	G
gi 21689936 emb AL390778.31 	Human DNA sequence from clone ...	38	9.4	
gi 32984072 dbj AK098863.1 	Oryza sativa (japonica cultivar...	38	9.4	U
gi 32982206 dbj AK072183.1 	Oryza sativa (japonica cultivar...	38	9.4	U

U
E

E
E
G
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G

Alignments

Get selected sequences Select all Deselect all

GIVE

Score = 417 bits (209), Expect = e-114
Identities = 270/285 (94%), Gaps = 6/285 (2%)
Strand = Plus / Plus

Query: 15 gcmggtgctgagcgccctagngcctcccttgccgcctccctcctctgcccgccgtagc 74
 || |||||
 Sbjct: 239 gcaggtgctgagcgccctagagcctcccttgccgcctccctcctctgcccgcccgagc 298

Query: 75 agtgcacat-gngtggttgaggtagatgggctcccgg-ccgggaggcggcggtggatgcg 132
 |||
 Sbjct: 299 agtgcacatgggggtgttgaggtagatgggctcccggcccgggaggcggcggtggatgcg 358

Query: 191 gtccccggttcagccatggggacctctccgagcagcagcaccgccctcggcctcctgcm- 249
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct: 419 gtccccggttcagccatggggacctctccgagcagcagcaccgccctc-gcctcctgcag 477

☐ >gi|37181727|gb|AY358304.1| **G|U** Homo sapiens clone DNA52594 DR6-TNFR (UNQ437) mR
Length = 3534

Query: 15 gcmggtgctgagcgccctagngcctcccttgccgcctccctcctctgcccgccgtagc 74
 ||
 Sbjct: 130 gcaggtgctgagcgccctagagcctcccttgccgcctccctcctctgcccgcccgagc 189

Query: 75 agtgcacat-gngtggttgaggttagatgggctcccgg-ccgggaggcgcggtggatgcg 132
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 190 agtgcacatgggggtgttgaggttagatgggctcccggccccgggaggcgcggtggatgcg 249

Query: 133 gcgctgggcag-mgcagccgccgattccagctgccccgcgcgcccc-ggccaccttgca 190
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 250 gcgctgggcagaagcagccgccgattccagctgccccgcgcgccccgggcacccctgca 309

Query: 191 gtccccgggttcagccatggggacctctccgagcagcagcaccgccctcggcctcctgcm- 249
 |||||
 Sbjct: 310 gtccccgggttcagccatggggacctctccgagcagcagcaccgccctc-gcctcctgcag 368

Query: 250 ccgcacgcgccgcgagccacagccacgatgatcgcgggctccct 294
 |||
 Sbjct: 369 ccgcacgcgccgcgagccacagccacgatgatcgcgggctccct 413

☐ >[gi|7022799|dbj|AK001504.1|](#) **GI|UE** Homo sapiens cDNA FLJ10642 fis, clone NT2RP200
 to Homo sapiens TNFR-related death receptor-6 mRNA
 Length = 2636

Score = 417 bits (209), Expect = e-114
Identities = 270/285 (94%), Gaps = 6/285 (2%)
Strand = Plus / Plus

Query: 15 gcmggtgctgagcgcccctagngcctcccttgccgcctccctcctctgcccgccgtagc 74
 || |||||
 Sbjct: 200 gcaggtgctgagcgcccctagagcctcccttgccgcctccctcctctgcccgccgcagc 259

Query: 75 agtgcacat-gngtggttgaggttagatgggctcccg-gcgggaggcggcggtggatgcg 132
 |||||
 Sbjct: 260 agtgcacatgggggttggttgaggttagatgggctcccgcccgaggcggcggtggatgcg 319

Query: 133 gcgctgggcag-mgcagccgccgattccagctgccccgcgcgcccc-ggccacctgcca 190
 |||||
 Sbjct: 320 gcgctgggcagaagcagccgccgattccagctgccccgcgcgccccggcgccccctgcca 379

Query: 191 gtccccggttcagccatggggacctctccgagcagcagcaccgccctcggcctcctgcm- 249
 |||||
 Sbjct: 380 gtccccggttcagccatggggacctctccgagcagcagcaccgccctc-gcctcctgcag 438

Query: 250 ccgcatcgcccgccgagccacagccacgatgatcgcgggctccct 294
 |||||
 Sbjct: 439 ccgcatcgcccgccgagccacagccacgatgatcgcgggctccct 483

☐ >gi|6478163|emb|AL096801.18|HSJ181J13 ☒ Human DNA sequence from clone RP1-181J13
 Contains the TNFRSF21 gene for tumor necrosis factor
 receptor superfamily superfamily member 21 (DR6) and a CpG
 Island, complete sequence
 Length = 118271

Score = 417 bits (209), Expect = e-114
 Identities = 270/285 (94%), Gaps = 6/285 (2%)
 Strand = Plus / Plus

Query: 15 gcmggtgctgagcgcccctagngcctcccttgccgcctccctcctctgcccgccgtagc 74
 || |||||
 Sbjct: 36762 gcaggtgctgagcgcccctagagcctcccttgccgcctccctcctctgcccgccgcagc 36821

Query: 75 agtgcacat-gngtggttgaggttagatgggctcccg-gcgggaggcggcggtggatgcg 132
 |||||
 Sbjct: 36822 agtgcacatgggggttggttgaggttagatgggctcccgcccgaggcggcggtggatgcg 36881

Query: 133 gcgctgggcag-mgcagccgccgattccagctgccccgcgcgcccc-ggccacctgcca 190
 |||||
 Sbjct: 36882 gcgctgggcagaagcagccgccgattccagctgccccgcgcgccccggcgccccctgcca 36941

Query: 191 gtccccggttcagccatggggacctctccgagcagcagcaccgccctcggcctcctgcm- 249
 |||||
 Sbjct: 36942 gtccccggttcagccatggggacctctccgagcagcagcaccgccctc-gcctcctgcag 37000

Query: 250 ccgcatcgcccgccgagccacagccacgatgatcgcgggctccct 294

|||||
Sbjct: 37001 ccgcatcgcccgccgagccacagccacgatgatcgcggtccct 37045

☐ >gi|15880636|emb|AJ336218.1|HSA336218 Homo sapiens genomic sequence surrounding
NL6-FL22C
Length = 666

Score = 409 bits (205), Expect = e-111
Identities = 269/285 (94%), Gaps = 6/285 (2%)
Strand = Plus / Plus

Query: 15 gcmggtgctgagcgcccctagngcctcccttgccgcctccctcctctgcccggccgtagc 74
|| |||||
Sbjct: 17 gcaggtgctgagcgcccctagagcctcccttgccgcctccctcctctgcccggccgtagc 76

Query: 75 agtgcacat-gngtggttgaggttagatgggctcccgg-ccgggaggcggcggtggatgag 132
||||| | |||||
Sbjct: 77 agtgcacatggggtggttgaggttagatgggctcccggcccgggaggcggcggtcgatgag 136

Query: 133 gcgctgggcag-mgcagccgcccattccagctgccccgcgcgccc-ggccaccttgaga 190
||||| |||||
Sbjct: 137 gcgctgggcagaagcagccgcccattccagctgccccgcgcgcccgggcccctgaga 196

Query: 191 gtccccgggttcagccatggggacctctccgagcagcagcaccgcccctcgccctcctgcm- 249
|||||
Sbjct: 197 gtccccgggttcagccatggggacctctccgagcagcagcaccgcccctc-gcctcctgag 255

Query: 250 ccgcatcgcccgccgagccacagccacgatgatcgcggtccct 294
|||||
Sbjct: 256 ccgcatcgcccgccgagccacagccacgatgatcgcggtccct 300

☐ >gi|15880407|emb|AJ335989.1|HSA335989 Homo sapiens genomic sequence surrounding
NL6-DN19C
Length = 693

Score = 325 bits (163), Expect = 3e-86
Identities = 257/283 (90%), Gaps = 6/283 (2%)
Strand = Plus / Plus

Query: 15 gcmggtgctgagcgcccctagngcctcccttgccgcctccctcctctgcccggccgtagc 74
|| |||||
Sbjct: 17 gcaggtgctgagcgcccctagagcctcccttgccgcctccctcctctgcccggccgtagc 76

Query: 75 agtgcacat-gngtggttgaggttagatgggctcccgg-ccgggaggcggcggtggatgag 132
||||| | |||||
Sbjct: 77 agtgcacatggggtggttgaggttagatgggctcccggcccgggaggcggcggtcgatgag 136

```

Query: 133 gcgctgggcag-mgcagccgccgattccagctgccccgcgcgcccc-ggccaccttgca 190
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 137 gcgctgggcagaaacagccgccgattccaactgccccgcgcgccccggcgccccctgca 196

Query: 191 gtccccgggttcagccatggggacctctccgagcagcagcaccgccctcggcctcctgc-m 249
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 197 gtccccgggttcagccatggggacctttccgagcagcagcaccctgcctc-gccttctgcaa 255

Query: 250 ccgcatcgcccgccgagccacagccacgatgatcgcggggtcc 292
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 256 ccgcatcgaccgccgagccacattcacgatgatcgctgggtcc 298

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☐ >gi|15868604|emb|AJ324225.1|HSA324225 Homo sapiens genomic sequence surrounding
NL1-ZP16C
Length = 762

Score = 269 bits (135), Expect = 2e-69
Identities = 202/221 (91%), Gaps = 4/221 (1%)
Strand = Plus / Plus

```

Query: 15 gcmggtgctgagcgcccctagngcctcccttgccgcctccctcctctgcccggccgtagc 74
          || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 17 gcaggtgctgagcgcccctagagcctcccttgccgcctccctcctctgcccggccgcagc 76

Query: 75 agtgcacat-gngtggttgaggttagatgggctcccgg-cggggaggcggcggtggatgcg 132
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 77 agtgcacatggggtggttgaggttagatgggctcccggccccgggaggcggcggtcgatgcg 136

Query: 133 gcgctgggcag-mgcagccgccgattccagctgccccgcgcgcccc-ggccaccttgca 190
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 137 gcgctgggcagaaagcagccgccgattccagctgccccgcgcgccccggcgccccctgca 196

Query: 191 gtccccgggttcagccatggggacctctccgagcagcagcac 231
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 197 gtcctgggctcagccatggggacctctgagaggagcagcac 237

```

☐ >gi|34783298|gb|BC017730.2| **GNIE** Homo sapiens tumor necrosis factor receptor su
mRNA (cDNA clone MGC:21476 IMAGE:3847246), complete cds
Length = 3238

Score = 166 bits (83), Expect = 3e-38
Identities = 98/101 (97%), Gaps = 2/101 (1%)
Strand = Plus / Plus

```

Query: 195 ccggttcagccatggggacctctccgagcagcagcaccgccctcggcctcctgcm-ccgc 253
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 1 ccggttcagccatggggacctctccgagcagcagcaccgccctcg-cctcctgcagccgc 59

```

Query: 254 atcgcccgccgagccacagccacgatgatcgcgggctccct 294
|||||
Sbjct: 60 atcgcccgccgagccacagccacgatgatcgcgggctccct 100

☐ >[gi|3549262|gb|AF068868.1|](#) **GUIE** Homo sapiens TNFR-related death receptor-6 (DR6)
Length = 1968

Score = 144 bits (72), Expect = 1e-31
Identities = 87/90 (96%), Gaps = 2/90 (2%)
Strand = Plus / Plus

Query: 206 atggggacctctccgagcagcagcaccgccctcggcctcctgcm-ccgcatcgcccgccg 264
|||||
Sbjct: 1 atggggacctctccgagcagcagcaccgccctcg-cctcctgcagccgcatcgcccgccg 59

Query: 265 agccacagccacgatgatcgcgggctccct 294
|||||
Sbjct: 60 agccacagccacgatgatcgcgggctccct 89

☐ >[gi|32880108|gb|BT009883.1|](#) Synthetic construct Homo sapiens tumor necrosis fact
superfamily, member 21 mRNA, partial cds
Length = 1968

Score = 144 bits (72), Expect = 1e-31
Identities = 87/90 (96%), Gaps = 2/90 (2%)
Strand = Plus / Plus

Query: 206 atggggacctctccgagcagcagcaccgccctcggcctcctgcm-ccgcatcgcccgccg 264
|||||
Sbjct: 1 atggggacctctccgagcagcagcaccgccctcg-cctcctgcagccgcatcgcccgccg 59

Query: 265 agccacagccacgatgatcgcgggctccct 294
|||||
Sbjct: 60 agccacagccacgatgatcgcgggctccct 89

☐ >[gi|30583678|gb|BT007420.1|](#) **GUIE** Homo sapiens tumor necrosis factor receptor su
mRNA, complete cds
Length = 1968

Score = 144 bits (72), Expect = 1e-31
Identities = 87/90 (96%), Gaps = 2/90 (2%)
Strand = Plus / Plus

Query: 206 atggggacctctccgagcagcagcaccgccctcggcctcctgcm-ccgcatcgcccgccg 264
|||||
Sbjct: 1 atggggacctctccgagcagcagcaccgccctcg-cctcctgcagccgcatcgcccgccg 59

Query: 265 agccacagccacgatgatcgcgggctccct 294
 |||||
 Sbjct: 60 agccacagccacgatgatcgcgggctccct 89

☐ >gi|55626753|ref|XM_518523.1| PREDICTED: Pan troglodytes tumor necrosis factor r
 superfamily, member 21 (LOC462749), mRNA
 Length = 2364

Score = 136 bits (68), Expect = 3e-29
 Identities = 86/90 (95%), Gaps = 2/90 (2%)
 Strand = Plus / Plus

Query: 206 atggggacctctccgagcagcagcaccgccctcggcctcctgcm-ccgcatcgcccgcg 264
 |||||
 Sbjct: 1 atggggacctctgagcagcagcaccgccctcg-cctcctgagccgcatcgcccgcg 59


Query: 265 agccacagccacgatgatcgcgggctccct 294
 |||||
 Sbjct: 60 agccacagccacgatgatcgcgggctccct 89

☐ >gi|15870715|emb|AJ326321.1|HSA326321 Homo sapiens genomic sequence surrounding
 Length = 713

Score = 122 bits (61), Expect = 5e-25
 Identities = 85/93 (91%), Gaps = 1/93 (1%)
 Strand = Plus / Plus

Query: 15 gcmggtgctgagcgcccctagngcctcccttgccgctccctcctctgcccgccgtagc 74
 || |||||
 Sbjct: 17 gcaggtgctgagcgcccatagagcctcccttgccgctccctcctctgcccgccgcagc 76

Query: 75 agtgcacat-gngtgttgaggtagatgggctc 106
 | |||||
 Sbjct: 77 aatgcacatggggtgttgaggtagattggctc 109

☐ >gi|34874517|ref|XM_236992.2|  Rattus norvegicus similar to death receptor 6
 Length = 2239

Score = 96.3 bits (48), Expect = 4e-17
 Identities = 87/97 (89%), Gaps = 3/97 (3%)
 Strand = Plus / Plus

Query: 73 gcagtgcacatgng-tgttgaggtagatgggctc-ccggccgggaggcggcggtggatg 130
 |||||
 Sbjct: 129 gcagtgcacatgggctgctggaggtagatgggctcaccgcccgtgaggcggcggtggatg 188

Query: 131 cggcgctgggcag-mgcagccgcccattccagctgcc 166
|||||
Sbjct: 189 cggcgctgggcagaaacagccaccgattccagctgcc 225

Score = 56.4 bits (28), Expect = 4e-05
Identities = 91/110 (82%), Gaps = 2/110 (1%)
Strand = Plus / Plus

Query: 186 tgcgagtgccccggttcagccatggggacctctccgagcagcagcaccgccctcgccctcc 245
||||| ||| || |||||
Sbjct: 252 tgcgagccccgggctcagccatggggacctccgcaagcagcatcaccgccctc-gcctct 310

Query: 246 tgcg-cgcgcatcgcccggcagccacagccacgatgatcgcgggctccct 294
||| ||||| ||| || ||||| ||| |||||
Sbjct: 311 tgcagccgcatcgcccggccaagtggagccacgatggtcgccggctccct 360

☐ >gi|31341673|ref|NM_178589.2| **GIU** Mus musculus tumor necrosis factor receptor su
(Tnfrsf21), mRNA
Length = 3628

Score = 88.3 bits (44), Expect = 9e-15
Identities = 86/97 (88%), Gaps = 3/97 (3%)
Strand = Plus / Plus

Query: 73 gcagtgcacatgng-tgttgaggtagatgggctc-ccggccgggaggcggcggtggatg 130
||||| ||| || ||||| ||| ||| |||||
Sbjct: 302 gcagtgcacatgggctgctggaggttagatgggctcaccgcccgtgaggcggcggtggatg 361

Query: 131 cggcgctgggcag-mgcagccgcccattccagctgcc 166
|||||
Sbjct: 362 cggcgctgggcagaaacagccaccaattccagctgcc 398

☐ >gi|26335926|dbj|AK043823.1| **GIU** Mus musculus 10 days neonate cortex cDNA, RIKEN
enriched library, clone:A830037A05 product:Death
Receptor 6, full insert sequence
Length = 3628

Score = 88.3 bits (44), Expect = 9e-15
Identities = 86/97 (88%), Gaps = 3/97 (3%)
Strand = Plus / Plus

Query: 73 gcagtgcacatgng-tgttgaggtagatgggctc-ccggccgggaggcggcggtggatg 130
||||| ||| || ||||| ||| ||| |||||
Sbjct: 302 gcagtgcacatgggctgctggaggttagatgggctcaccgcccgtgaggcggcggtggatg 361

Query: 131 cggcgctgggcag-mgcagccgcccattccagctgcc 166
|||||
Sbjct: 362 cggcgctgggcagaaacagccaccaattccagctgcc 398

☐ >gi|16741136|gb|BC016420.1| **GU E** Mus musculus tumor necrosis factor receptor su
 mRNA (cdna clone MGC:25901 IMAGE:4220624), complete cds
 Length = 2748

Score = 86.3 bits (43), Expect = 4e-14
Identities = 85/96 (88%), Gaps = 3/96 (3%)
Strand = Plus / Plus

Query: 73 gcagtgcacatgng-tgttgaggtagatgggctc-ccggccgggagggcggcggtggatg 130
|||||
Sbjct: 249 gcagtgcacatgggctgctggaggtagatgggctcaccgcccgtagggcggcggtggatg 308

```
Query: 131  cggcgctgggcag-mgcagccgcgattccagctgc 165
           ||||| ||||| ||||| ||||| |||||
Sbjct: 309  cggcgctgggcagaaacagccaccaattccagctgc 344
```

❑ >[gi|26329206|dbj|AK033529.1|](#) **GU** Mus musculus adult male colon cDNA, RIKEN full-library, clone:9030604G24 product:Death Receptor 6, full insert sequence
Length = 3597

Score = 82.3 bits (41), Expect = 6e-13
Identities = 71/79 (89%), Gaps = 2/79 (2%)
Strand = Plus / Plus

Query: 90 tggaggtagatgggctc-ccggccgggaggcggcgggtggatgcggcgctgggcag-mgca 147
|||||
Sbjct: 295 tggaggtagatgggctcaccgcccgtagggcggcgggtggatgcggcgctgggcagaaaca 354

```
Query: 148 gccgccgattccagctgcc 166
      ||| || |||||
Sbjct: 355 gccaccaattccagctgcc 373
```

☐ >gi|15877202|emb|AJ332784.1|HSA332784 Homo sapiens genomic sequence surrounding
 NL6-DB13C
 Length = 670

Score = 52.4 bits (26), Expect = 6e-04
Identities = 47/55 (85%)
Strand = Plus / Plus

Query: 15 gcmggtgctgagcgccctagngcctcccttgccgcctccctcctctgcccgcc 69
 |||
 Sbjct: 17 gcaggtgcttagcgccgctagagcctcccttgccgactctcttcttgcccgcc 71

☐ >gi|17432071|emb|AL646086.1| ☒ Ralstonia solanacearum GMI1000 megaplasmid, compl
11/11
Length = 92509

Score = 44.4 bits (22), Expect = 0.15
Identities = 22/22 (100%)
Strand = Plus / Plus

Query: 222 gcagcagcaccgccctcggcct 243
|||||
Sbjct: 11349 gcagcagcaccgccctcggcct 11370

☐ >gi|56178122|gb|AE017340.1| ☒ Idiomarina loihiensis L2TR, complete genome
Length = 2839318

Score = 42.4 bits (21), Expect = 0.59
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 107 ccggccgggaggcggtgg 127
|||||
Sbjct: 25553 ccggccgggaggcggtgg 25573

☐ >gi|22795236|gb|AC127460.2| ☒ Homo sapiens chromosome 5 clone RP11-689B23, compl
Length = 115293

Score = 42.4 bits (21), Expect = 0.59
Identities = 24/25 (96%)
Strand = Plus / Plus

Query: 100 tgggctcccggccgggaggcggcg 124
|||||
Sbjct: 37541 tgggctcccggccggcaggcggcg 37565

☐ >gi|14625084|gb|AC084380.8|AC084380 ☒ Oryza sativa chromosome 3 BAC OSJNBa0090P2
sequence
Length = 126164

Score = 42.4 bits (21), Expect = 0.59
Identities = 21/21 (100%)
Strand = Plus / Minus

Query: 46 gccgcctccctcctctgcccg 66
|||||
Sbjct: 35828 gccgcctccctcctctgcccg 35808

☐ >gi|33879154|gb|BC021165.2| **GU** Homo sapiens zinc finger protein 503, mRNA (cDNA IMAGE:3830632), complete cds
Length = 2446

Score = 40.4 bits (20), Expect = 2.3
Identities = 23/24 (95%)
Strand = Plus / Plus

Query: 110 gccgggaggcggcggtggatgcgg 133
|||||
Sbjct: 670 gccgggaggcggcggtggaggcgg 693

☐ >gi|33870187|gb|BC013011.2| **GU** Homo sapiens zinc finger protein 503, mRNA (cDNA IMAGE:3604473), complete cds
Length = 2446

Score = 40.4 bits (20), Expect = 2.3
Identities = 23/24 (95%)
Strand = Plus / Plus

Query: 110 gccgggaggcggcggtggatgcgg 133
|||||
Sbjct: 670 gccgggaggcggcggtggaggcgg 693

☐ >gi|34871182|ref|XM_343874.1| **GU** Rattus norvegicus similar to fibrillarin; 34-k scleroderma antigen; RNA, U3 small nucleolar interacting protein 1 (LOC363563), mRNA
Length = 882

Score = 40.4 bits (20), Expect = 2.3
Identities = 20/20 (100%)
Strand = Plus / Minus

Query: 37 gcctcccttgccgcctccct 56
|||||
Sbjct: 66 gcctcccttgccgcctccct 47

☐ >gi|25453488|gb|AY057439.2| Azotobacter vinelandii GroEL (groEL) and group II in open reading frame genes, complete cds; and probable pseudouridylate synthase (rsuA) gene, partial cds
Length = 5054

Score = 40.4 bits (20), Expect = 2.3
Identities = 20/20 (100%)
Strand = Plus / Minus

Query: 170 cgcgccccggccaccttgcg 189
|||||
Sbjct: 2001 cgcgccccggccaccttgcg 1982

☐ >gi|52421840|gb|CP000011.1| ☒ Burkholderia mallei ATCC 23344 chromosome 2, compl
Length = 2325379

Score = 40.4 bits (20), Expect = 2.3
Identities = 20/20 (100%)
Strand = Plus / Plus

Query: 122 cggtaggatgcggcgctgggc 141
|||||
Sbjct: 943204 cggtaggatgcggcgctgggc 943223

Score = 40.4 bits (20), Expect = 2.3
Identities = 20/20 (100%)
Strand = Plus / Plus

Query: 122 cggtaggatgcggcgctgggc 141
|||||
Sbjct: 468147 cggtaggatgcggcgctgggc 468166

Score = 34.4 bits (17), Expect = 149
Identities = 17/17 (100%)
Strand = Plus / Minus

Query: 218 ccgagcagcagcaccgc 234
|||||
Sbjct: 1853112 ccgagcagcagcaccgc 1853096

Score = 34.4 bits (17), Expect = 149
Identities = 17/17 (100%)
Strand = Plus / Minus

Query: 218 ccgagcagcagcaccgc 234
|||||
Sbjct: 1526326 ccgagcagcagcaccgc 1526310

Score = 32.4 bits (16), Expect = 594
Identities = 16/16 (100%)
Strand = Plus / Plus

Query: 218 ccgagcagcagcaccg 233
|||||
Sbjct: 2150293 ccgagcagcagcaccg 2150308